



SEQUENCE LISTING

<110> Arkowitz, Robert A
Nern, Peter MA

<120> NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

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<141> 2002-01-21

<150> 09/168,474

<151> 1998-10-08

<150> 08/951,141

<151> 1997-10-15

<150> 09/529,106

<151> 2000-04-07

<150> US 09/732,180

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<150> US 60/169,699

<151> 1999-12-07

<150> PCT/GB98/03033

<151> 1998-10-08

<150> 9812793.9

<151> 1998-06-12

<150> 9721357.3

<151> 1997-10-08

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Saccharomyces cerevisiae

<220>

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tttgcattta	acgatgagga	gcttttcact	atatccgacg	tttttgccaa	ctcgacgtcc	180
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<210> 2

<211> 76

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

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<400> 2

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 3

<211> 228

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: nucleic acid

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tttgatttta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctgggtca aagtgctaga agtagtagaa acgctaata attccagc 228

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<211> 76

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: amino acid

<400> 4

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 5

<211> 228

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctgggtca aagtgctaga agtagtagaa acgctaataa attccagc 228

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<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

<400> 6
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15
Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 7
<211> 228
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: nucleic acid

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tttgcattta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctgggtca aagtgctaga agtagtagaa acgctaataa attccagc 228

<210> 8
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

<400> 8
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 20 25 30
 Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
 35 40 45
 Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
 50 55 60
 Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
 65 70 75

<210> 9
 <211> 392
 <212> PRT
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: amino acid

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 Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
 35 40 45
 Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
 50 55 60
 Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
 65 70 75 80
 His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
 85 90 95
 Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
 100 105 110
 Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
 115 120 125
 Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
 130 135 140
 Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
 145 150 155 160
 Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
 165 170 175
 Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
 180 185 190
 Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe

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Asp	Lys	Val	Phe	Ile	Ser	Thr	Thr	Asn	Ser	Ser	Ser	Glu	Pro	Glu	Arg		
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Glu	Phe	Glu	Val	Tyr	Leu	Phe	Glu	Lys	Ile	Ile	Ile	Leu	Phe	Ser	Glu		
225					230					235					240		
Val	Val	Thr	Lys	Lys	Ser	Ala	Ser	Ser	Leu	Ile	Leu	Lys	Lys	Lys	Ser		
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Ser	Thr	Ser	Ala	Ser	Ile	Ser	Ala	Ser	Asn	Ile	Thr	Asp	Asn	Asn	Gly		
			260					265					270				
Ser	Pro	His	His	Ser	Tyr	His	Lys	Arg	His	Ser	Asn	Ser	Ser	Ser	Ser		
		275					280					285					
Asn	Asn	Ile	His	Leu	Ser	Ser	Ser	Ser	Ala	Ala	Ala	Ile	Ile	His	Ser		
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Ser	Thr	Asn	Ser	Ser	Asp	Asn	Asn	Ser	Asn	Asn	Ser	Ser	Ser	Ser	Ser		
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Leu	Phe	Lys	Leu	Ser	Ala	Asn	Glu	Pro	Lys	Leu	Asp	Leu	Arg	Gly	Arg		
				325					330					335			
Ile	Met	Ile	Met	Asn	Leu	Asn	Gln	Ile	Ile	Pro	Gln	Asn	Asn	Arg	Ser		
			340					345					350				
Leu	Asn	Ile	Thr	Trp	Glu	Ser	Ile	Lys	Glu	Gln	Gly	Asn	Phe	Leu	Leu		
		355				360					365						
Lys	Phe	Lys	Asn	Glu	Glu	Thr	Arg	Asp	Asn	Trp	Ser	Ser	Cys	Leu	Gln		
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Gln	Leu	Ile	His	Asp	Leu	Lys	Asn										
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<212> DNA
<213> Saccharomyces cerevisiae
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gccagaacag	agagtaaatc	gcttcagctg	caaataataa	aagcaaaaaa	caagatacaa	180
gatgcaagct	tattccagat	ggccaacaaa	gttacttcgt	tgaccaaaaa	taagatcaac	240
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cgagattcaa	aacgtatttt	gagtgcaagt	caagatggct	tatgcttat	atgggacagt	360
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agagtttcga	aagaaaacag	agtagcgcaa	acagttgcgt	caattttcaa	aggacatact	540
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ttaggtgatg	ttttggcatt	agctattctc	gaagagccaa	acttagaaaa	ttcttcgaac	720
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Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
 225 230 235 240
 Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
 245 250 255
 Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
 260 265 270
 Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
 275 280 285
 Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
 290 295 300
 Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
 305 310 315 320
 Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
 325 330 335
 Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
 340 345 350
 Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
 355 360 365
 Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
 370 375 380
 Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
 385 390 395 400
 Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
 405 410 415
 Trp Ser Pro Gly Tyr Gln
 420

<210> 12
 <211> 1269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid

<400> 12
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 gccagacaag agagtaaaca gcttcagtct caaataaata aagcaaaaaca caagatacaa 180
 gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
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210 215 220

Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
 225 230 235 240

Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
 245 250 255

Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
 260 265 270

Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
 275 280 285

Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
 290 295 300

Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
 305 310 315 320

Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
 325 330 335

Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
 340 345 350

Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
 355 360 365

Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
 370 375 380

Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
 385 390 395 400

Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
 405 410 415

Trp Ser Pro Gly Tyr Gln
 420

<210> 14
 <211> 1269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence

<400> 14
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 gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
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acattcgcta gctgtggatc agacgggtat acttacatat gggatagcag atctccgtcc 780
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1269

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<210> 15

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid sequence

<400> 15

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Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
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Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
      20             25             30

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Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
    35             40             45

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```

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
    50             55             60

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```

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
    65             70             75             80

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```

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
      85             90             95

```

```

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
    100             105             110

```

```

Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
    115             120             125

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```

Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
    130             135             140

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```

Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
    145             150             155             160

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```

Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
    165             170             175

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```

Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
    180             185             190

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His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile

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Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser 245 250 255		
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile 260 265 270		
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser 275 280 285		
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile 290 295 300		
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro 305 310 315 320		
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln 325 330 335		
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val 340 345 350		
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr 355 360 365		
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly 370 375 380		
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro 385 390 395 400		
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile 405 410 415		
Trp Ser Pro Gly Tyr Gln 420		

<210> 16

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid
sequence

<400> 16

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
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<210> 17

<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 17
Gln Asn Leu Tyr Phe Gln Gly
1 5

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 18
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys
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Lys Ser Ile

<210> 19
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 19
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 20
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 21

<211> 19
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<223>

<400> 21
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 22
<211> 19
<212> PRT
<213> Human

<220>
<223>

<400> 22
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
1 5 10 15

Lys Thr Ile

<210> 23
<211> 2535
<212> DNA
<213> *Candida albicans*

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ttcaataaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180
aaactacaaa aaatccctgg catggaacca tttttgaacc aagctttcaa tcaggctgaa 240
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Gln	Ile	Pro	Val	Val	Ser	Ser	Asp	Asp	Leu	Arg	Ile	Cys	Lys	Lys	Ser	195	200	205
Val	Tyr	Asp	Phe	Leu	Ile	Ala	Val	Lys	Thr	Gln	Leu	Asn	Phe	Asp	Asp	210	215	220
Glu	Asn	Met	Phe	Thr	Ile	Ser	Asn	Val	Phe	Ser	Asp	Asn	Ala	Gln	Asp	225	230	235
Leu	Ile	Lys	Ile	Ile	Asp	Val	Ile	Asn	Lys	Leu	Leu	Ala	Glu	Tyr	Ser	245	250	255
Asp	Ala	Ser	Asp	Ser	Gly	Gly	Gly	Asp	Glu	Asp	Val	Asn	Met	Asp	Val	260	265	270
Gln	Ile	Thr	Asp	Glu	Arg	Ser	Lys	Val	Phe	Arg	Glu	Ile	Ile	Glu	Thr	275	280	285
Glu	Arg	Lys	Tyr	Val	Gln	Asp	Leu	Glu	Leu	Met	Cys	Lys	Tyr	Arg	Gln	290	295	300
Asp	Leu	Ile	Glu	Ala	Glu	Asn	Leu	Ser	Ser	Glu	Gln	Ile	His	Leu	Leu	305	310	315
Phe	Pro	Asn	Leu	Asn	Glu	Ile	Ile	Asp	Phe	Gln	Arg	Arg	Phe	Leu	Asn	325	330	335
Gly	Leu	Glu	Cys	Asn	Ile	Asn	Val	Pro	Ile	Arg	Tyr	Gln	Arg	Ile	Gly	340	345	350
Ser	Val	Phe	Ile	His	Ala	Ser	Leu	Gly	Pro	Phe	Asn	Ala	Tyr	Glu	Pro	355	360	365
Trp	Thr	Ile	Gly	Gln	Leu	Thr	Ala	Ile	Asp	Leu	Ile	Asn	Lys	Glu	Ala	370	375	380
Ala	Asn	Leu	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Asp	Pro	Gly	Phe	Glu	Leu	385	390	395
Gln	Ser	Tyr	Ile	Leu	Lys	Pro	Ile	Gln	Arg	Leu	Cys	Lys	Tyr	Pro	Leu	405	410	415
Leu	Leu	Lys	Glu	Leu	Ile	Lys	Thr	Ser	Pro	Glu	Tyr	Ser	Lys	Gln	Asp	420	425	430
Pro	His	Gly	Ser	Ser	Ser	Ser	Thr	Ser	Phe	Asn	Glu	Leu	Leu	Val	Ala	435	440	445
Lys	Thr	Ala	Met	Lys	Glu	Leu	Ala	Asn	Gln	Val	Asn	Glu	Ala	Gln	Arg	450	455	460
Arg	Ala	Glu	Asn	Ile	Glu	His	Leu	Glu	Lys	Leu	Lys	Glu	Arg	Val	Gly	465	470	475
Asn	Trp	Arg	Gly	Phe	Asn	Leu	Asp	Ala	Gln	Gly	Glu	Leu	Leu	Phe	His	485	490	495
Gly	Gln	Val	Gly	Val	Lys	Asp	Ala	Glu	Asn	Glu	Lys	Glu	Tyr	Val	Ala	500	505	510

Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp Asp Thr
 515 520 525
 Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys
 530 535 540
 Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu
 545 550 555 560
 Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys
 565 570 575
 Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr
 580 585 590
 Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly
 595 600 605
 Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu
 610 615 620
 Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His
 625 630 635 640
 Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala
 645 650 655
 Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr
 660 665 670
 Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His
 675 680 685
 Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser
 690 695 700
 Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe
 705 710 715 720
 Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met
 725 730 735
 Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys
 740 745 750
 Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala
 755 760 765
 Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile
 770 775 780
 Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr
 785 790 795 800
 Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp
 805 810 815
 Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser
 820 825 830
 Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser

835

840

<210> 25

<211> 22

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser
 1 5 10 15

Ile Tyr Asp Phe Ile Leu
 20

<210> 26

<211> 22

<212> PRT

<213> *Candida albicans*

<400> 26

Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
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Val Tyr Asp Phe Leu Ile
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<210> 27

<211> 854

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 27

Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu
 1 5 10 15

Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val
 20 25 30

Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala
 35 40 45

Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu
 50 55 60

Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu
 65 70 75 80

Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala
 85 90 95

Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ile
 100 105 110

Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn
 115 120 125

Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe
 130 135 140

Ser 145	Met	Gly	Ile	Leu	Pro 150	Ile	Thr	Met	Asp	Cys 155	Asp	Pro	Val	Thr	Gln 160
Leu	Ser	Gln	Leu	Phe 165	Gln	Gln	Gly	Ala	Pro 170	Leu	Cys	Ile	Leu	Phe 175	Asn
Ser	Val	Lys	Pro 180	Gln	Phe	Lys	Leu	Pro 185	Val	Ile	Ala	Ser	Asp 190	Asp	Leu
Lys	Val	Cys 195	Lys	Lys	Ser	Ile	Tyr 200	Asp	Phe	Ile	Leu	Gly 205	Cys	Lys	Lys
His	Phe 210	Ala	Phe	Asn	Asp	Glu 215	Glu	Leu	Phe	Thr	Ile 220	Ser	Asp	Val	Phe
Ala 225	Asn	Ser	Thr	Ser	Gln 230	Leu	Val	Lys	Val	Leu 235	Glu	Val	Val	Glu	Thr 240
Leu	Met	Asn	Ser	Ser 245	Pro	Thr	Ile	Phe	Pro 250	Ser	Lys	Ser	Lys	Thr 255	Gln
Gln	Ile	Met	Asn 260	Ala	Glu	Asn	Gln	His 265	Arg	His	Gln	Pro	Gln 270	Gln	Ser
Ser	Lys	Lys 275	His	Asn	Glu	Tyr	Val 280	Lys	Ile	Ile	Lys	Glu 285	Phe	Val	Ala
Thr	Glu 290	Arg	Lys	Tyr	Val	His 295	Asp	Leu	Glu	Ile	Leu 300	Asp	Lys	Tyr	Arg
Gln 305	Gln	Leu	Leu	Asp	Ser 310	Asn	Leu	Ile	Thr	Ser 315	Glu	Glu	Leu	Tyr	Met 320
Leu	Phe	Pro	Asn 325	Leu	Gly	Asp	Ala	Ile	Asp 330	Phe	Gln	Arg	Arg	Phe 335	Leu
Ile	Ser	Leu	Glu 340	Ile	Asn	Ala	Leu	Val 345	Glu	Pro	Ser	Lys	Gln 350	Arg	Ile
Gly	Ala 355	Leu	Phe	Met	His	Ser	Lys 360	His	Phe	Phe	Lys	Leu 365	Tyr	Glu	Pro
Trp 370	Ser	Ile	Gly	Gln	Asn	Ala 375	Ala	Ile	Glu	Phe	Leu 380	Ser	Ser	Thr	Leu
His 385	Lys	Met	Arg	Val	Asp 390	Glu	Ser	Gln	Arg	Phe 395	Ile	Ile	Asn	Asn	Lys 400
Leu	Glu	Leu	Gln 405	Ser	Phe	Leu	Tyr	Lys	Pro 410	Val	Gln	Arg	Leu	Cys 415	Arg
Tyr	Pro	Leu	Leu 420	Val	Lys	Glu	Leu	Leu 425	Ala	Glu	Ser	Ser	Asp 430	Asp	Asn
Asn	Thr	Lys 435	Glu	Leu	Glu	Ala	Ala 440	Leu	Asp	Ile	Ser	Lys 445	Asn	Ile	Ala
Arg	Ser 450	Ile	Asn	Glu	Asn	Gln 455	Arg	Arg	Thr	Glu	Asn 460	His	Gln	Val	Val

Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser
 465 470 475 480
 Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr
 485 490 495
 Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu
 500 505 510
 Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser
 515 520 525
 Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala
 530 535 540
 Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys
 545 550 555 560
 Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser
 565 570 575
 Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn Ser Ser Asp Asn Asn
 580 585 590
 Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu
 595 600 605
 Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln
 610 615 620
 Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile
 625 630 635 640
 Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg
 645 650 655
 Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn
 660 665 670
 Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser
 675 680 685
 Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr
 690 695 700
 Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe
 705 710 715 720
 Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg
 725 730 735
 Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn
 740 745 750
 Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr
 755 760 765
 Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu
 770 775 780
 Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser

785						790						795						800
Lys	Ile	Ser	Asn	Thr	His	Asn	Asn	Asn	Ile	Ser	Pro	Ile	Thr	Lys	Ile			
				805					810					815				
Lys	Tyr	Gln	Asp	Glu	Asp	Gly	Asp	Phe	Val	Val	Leu	Gly	Ser	Asp	Glu			
				820					825					830				
Asp	Trp	Asn	Val	Ala	Lys	Glu	Met	Leu	Ala	Glu	Asn	Asn	Glu	Lys	Phe			
				835					840					845				
Leu	Asn	Ile	Arg	Leu	Tyr													
				850														

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<210> 28
<211> 837
<212> PRT
<213> Saccharomyces cerevisiae
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<400> 28																
Ser	Gly	Thr	Ser	Leu	Ser	Asp	Leu	Lys	Pro	Lys	Pro	Ser	Ala	Thr	Ser	
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Ile	Ser	Ile	Pro	Met	Gln	Asn	Val	Met	Asn	Lys	Pro	Val	Thr	Glu	Gln	
			20					25					30			
Asp	Ser	Leu	Phe	His	Ile	Cys	Ala	Asn	Ile	Arg	Lys	Arg	Leu	Glu	Val	
		35					40					45				
Leu	Pro	Gln	Leu	Lys	Pro	Phe	Leu	Gln	Leu	Ala	Tyr	Gln	Ser	Ser	Glu	
	50					55					60					
Val	Leu	Ser	Glu	Arg	Gln	Ser	Leu	Leu	Leu	Ser	Gln	Lys	Gln	His	Gln	
65					70					75					80	
Glu	Leu	Leu	Lys	Ser	Asn	Gly	Ala	Asn	Arg	Asp	Ser	Ser	Asp	Leu	Ala	
				85					90					95		
Pro	Thr	Leu	Arg	Ser	Ser	Ser	Ile	Ser	Thr	Ala	Thr	Ser	Leu	Met	Ser	
			100					105					110			
Met	Glu	Gly	Ile	Ser	Tyr	Thr	Asn	Ser	Asn	Pro	Ser	Ala	Thr	Pro	Asn	
		115					120					125				
Met	Glu	Asp	Thr	Leu	Leu	Thr	Phe	Ser	Met	Gly	Ile	Leu	Pro	Ile	Thr	
	130					135					140					
Met	Asp	Cys	Asp	Pro	Val	Thr	Gln	Leu	Ser	Gln	Leu	Phe	Gln	Gln	Gly	
145					150					155					160	
Ala	Pro	Leu	Cys	Ile	Leu	Phe	Asn	Ser	Val	Lys	Pro	Gln	Phe	Lys	Leu	
				165					170					175		
Pro	Val	Ile	Ala	Ser	Asp	Asp	Leu	Lys	Val	Cys	Lys	Lys	Ser	Ile	Tyr	
			180					185					190			
Asp	Phe	Ile	Leu	Gly	Cys	Lys	Lys	His	Phe	Ala	Phe	Asn	Asp	Glu	Glu	
		195					200					205				
Leu	Phe	Thr	Ile	Ser	Asp	Val	Phe	Ala	Asn	Ser	Thr	Ser	Gln	Leu	Val	

210	215	220
Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile 225 230 235 240		
Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln 245 250 255		
His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val 260 265 270		
Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp 275 280 285		
Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu 290 295 300		
Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala 305 310 315 320		
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu 325 330 335		
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys 340 345 350		
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala 355 360 365		
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser 370 375 380		
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr 385 390 395 400		
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu 405 410 415		
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala 420 425 430		
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg 435 440 445		
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val 450 455 460		
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe 465 470 475 480		
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg 485 490 495		
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu 500 505 510		
Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser 515 520 525		
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly 530 535 540		

Ser Pro His His Ser Tyr His Lys Arg His Ser Asn Ser Ser Ser Ser
 545 550 555 560
 Asn Asn Ile His Leu Ser Ser Ser Ser Ala Ala Ala Ile Ile His Ser
 565 570 575
 Ser Thr Asn Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser
 580 585 590
 Leu Phe Lys Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg
 595 600 605
 Ile Met Ile Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser
 610 615 620
 Leu Asn Ile Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu
 625 630 635 640
 Lys Phe Lys Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln
 645 650 655
 Gln Leu Ile His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His
 660 665 670
 Ser Ser Thr Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met
 675 680 685
 Ser Pro Thr Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln
 690 695 700
 Thr His Asp Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val
 705 710 715 720
 Ser Asp Val Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser
 725 730 735
 Glu Ile Lys Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser
 740 745 750
 Ser Ile Leu Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser
 755 760 765
 Ser Ser Glu Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp
 770 775 780
 Asp Leu Ile Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn
 785 790 795 800
 Asn Ile Ser Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp
 805 810 815
 Phe Val Val Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu Met
 820 825 830
 Leu Ala Glu Asn Asn
 835

<210> 29
 <211> 813

<212> PRT

<213> Candida albicans

<400> 29

Ser	Thr	Ser	Ser	Leu	Asn	Ser	Val	Ser	Thr	Val	Ser	Ser	Ser	Arg	Ile
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Val	Ser	Ser	Gly	Pro	Val	Asn	Ile	Asn	Asn	Phe	Asn	Lys	Pro	Ser	Thr
			20					25					30		
Pro	Lys	Asp	His	Leu	Phe	Tyr	Arg	Cys	Glu	Ser	Leu	Lys	Arg	Lys	Leu
		35					40					45			
Gln	Lys	Ile	Pro	Gly	Met	Glu	Pro	Phe	Leu	Asn	Gln	Ala	Phe	Asn	Gln
	50					55					60				
Ala	Glu	Gln	Leu	Ser	Glu	Gln	Gln	Ala	Leu	Ala	Leu	Ala	Gln	Glu	Arg
65					70				75						80
Ser	Asn	Gly	Asn	Gly	His	Ser	Asn	Gly	Lys	Arg	His	Gln	Ser	Leu	Asp
				85					90						95
Gly	Ala	Met	Asn	Arg	Leu	Ser	Val	Gly	Ser	Asp	Ser	Ser	Ser	Ile	Gln
			100					105						110	
Gly	Ser	Leu	Thr	Arg	Met	Ala	Thr	Asn	Ala	Ser	Thr	Ser	Ser	Leu	Ile
		115					120						125		
Ser	Gly	Met	Pro	Asn	Asn	Asn	Thr	Leu	Phe	Thr	Phe	Thr	Ala	Gly	Val
	130					135					140				
Leu	Pro	Ala	Asn	Ile	Ser	Val	Asp	Pro	Ala	Thr	His	Leu	Trp	Lys	Leu
145					150					155					160
Phe	Gln	Gln	Gly	Ala	Pro	Phe	Cys	Val	Leu	Ile	Asn	His	Ile	Leu	Pro
				165					170					175	
Asp	Ser	Gln	Ile	Pro	Val	Val	Ser	Ser	Asp	Asp	Leu	Arg	Ile	Cys	Lys
			180					185					190		
Lys	Ser	Val	Tyr	Asp	Phe	Leu	Ile	Ala	Val	Lys	Thr	Gln	Leu	Asn	Phe
		195					200					205			
Asp	Asp	Glu	Asn	Met	Phe	Thr	Ile	Ser	Asn	Val	Phe	Ser	Asp	Asn	Ala
	210					215					220				
Gln	Asp	Leu	Ile	Lys	Ile	Ile	Asp	Val	Ile	Asn	Lys	Leu	Leu	Ala	Glu
225					230					235					240
Tyr	Ser	Asp	Ala	Ser	Asp	Ser	Gly	Gly	Gly	Asp	Glu	Asp	Val	Asn	Met
			245					250						255	
Asp	Val	Gln	Ile	Thr	Asp	Glu	Arg	Ser	Lys	Val	Phe	Arg	Glu	Ile	Ile
			260					265					270		
Glu	Thr	Glu	Arg	Lys	Tyr	Val	Gln	Asp	Leu	Glu	Leu	Met	Cys	Lys	Tyr
		275					280					285			
Arg	Gln	Asp	Leu	Ile	Glu	Ala	Glu	Asn	Leu	Ser	Ser	Glu	Gln	Ile	His
	290					295						300			

Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe
 305 310 315 320
 Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg
 325 330 335
 Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr
 340 345 350
 Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys
 355 360 365
 Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe
 370 375 380
 Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr
 385 390 395 400
 Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys
 405 410 415
 Gln Asp Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu
 420 425 430
 Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala
 435 440 445
 Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg
 450 455 460
 Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu
 465 470 475 480
 Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr
 485 490 495
 Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp
 500 505 510
 Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr
 515 520 525
 Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu
 530 535 540
 Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu
 545 550 555 560
 Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro
 565 570 575
 Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu
 580 585 590
 Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln
 595 600 605
 Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
 610 615 620
 Ile His Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp

625		630		635		640
Ser Ala Ile Tyr Asp	Tyr Thr Gly Ile Ser	Thr Ser Pro Val Asn	Gln			
645	650	655				
Ser Thr Gln Gln Gln Tyr Tyr Asp	His Arg Gly Ser His Ser Ser Arg					
660	665	670				
His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val						
675	680	685				
Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp						
690	695	700				
Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser						
705	710	715				720
Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala						
725	730	735				
Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val						
740	745	750				
Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln						
755	760	765				
Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu						
770	775	780				
Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp						
785	790	795				800
Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp						
805	810					

<210> 30
 <211> 684
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 30
Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
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Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
20 25 30
Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
35 40 45
Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr
50 55 60
Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
65 70 75 80
Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
85 90 95
Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His

100										105					110						
Gln	Pro	Gln	Gln	Ser	Ser	Lys	Lys	His	Asn	Glu	Tyr	Val	Lys	Ile	Ile						
		115					120					125									
Lys	Glu	Phe	Val	Ala	Thr	Glu	Arg	Lys	Tyr	Val	His	Asp	Leu	Glu	Ile						
	130					135					140										
Leu	Asp	Lys	Tyr	Arg	Gln	Gln	Leu	Leu	Asp	Ser	Asn	Leu	Ile	Thr	Ser						
145					150					155					160						
Glu	Glu	Leu	Tyr	Met	Leu	Phe	Pro	Asn	Leu	Gly	Asp	Ala	Ile	Asp	Phe						
				165					170					175							
Gln	Arg	Arg	Phe	Leu	Ile	Ser	Leu	Glu	Ile	Asn	Ala	Leu	Val	Glu	Pro						
			180					185					190								
Ser	Lys	Gln	Arg	Ile	Gly	Ala	Leu	Phe	Met	His	Ser	Lys	His	Phe	Phe						
		195					200					205									
Lys	Leu	Tyr	Glu	Pro	Trp	Ser	Ile	Gly	Gln	Asn	Ala	Ala	Ile	Glu	Phe						
	210					215					220										
Leu	Ser	Ser	Thr	Leu	His	Lys	Met	Arg	Val	Asp	Glu	Ser	Gln	Arg	Phe						
225					230					235					240						
Ile	Ile	Asn	Asn	Lys	Leu	Glu	Leu	Gln	Ser	Phe	Leu	Tyr	Lys	Pro	Val						
				245					250					255							
Gln	Arg	Leu	Cys	Arg	Tyr	Pro	Leu	Leu	Val	Lys	Glu	Leu	Leu	Ala	Glu						
			260					265					270								
Ser	Ser	Asp	Asp	Asn	Asn	Thr	Lys	Glu	Leu	Glu	Ala	Ala	Leu	Asp	Ile						
		275					280					285									
Ser	Lys	Asn	Ile	Ala	Arg	Ser	Ile	Asn	Glu	Asn	Gln	Arg	Arg	Thr	Glu						
	290					295					300										
Asn	His	Gln	Val	Val	Lys	Lys	Leu	Tyr	Gly	Arg	Val	Val	Asn	Trp	Lys						
305					310					315					320						
Gly	Tyr	Arg	Ile	Ser	Lys	Phe	Gly	Glu	Leu	Leu	Tyr	Phe	Asp	Lys	Val						
				325					330					335							
Phe	Ile	Ser	Thr	Thr	Asn	Ser	Ser	Ser	Glu	Pro	Glu	Arg	Glu	Phe	Glu						
			340					345					350								
Val	Tyr	Leu	Phe	Glu	Lys	Ile	Ile	Ile	Leu	Phe	Ser	Glu	Val	Val	Thr						
		355					360					365									
Lys	Lys	Ser	Ala	Ser	Ser	Leu	Ile	Leu	Lys	Lys	Lys	Ser	Ser	Thr	Ser						
	370	</																			

Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys
 435 440 445
 Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile
 450 455 460
 Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile
 465 470 475 480
 Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys
 485 490 495
 Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile
 500 505 510
 His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr
 515 520 525
 Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr
 530 535 540
 Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp
 545 550 555 560
 Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val
 565 570 575
 Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys
 580 585 590
 Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu
 595 600 605
 Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu
 610 615 620
 Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile
 625 630 635 640
 Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser
 645 650 655
 Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val
 660 665 670
 Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu
 675 680

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 <212> PRT
 <213> Schizosaccharomyces pombe

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Ser Ser Val Ser Leu Glu Asn Thr Asn Val Cys Lys Ala Ser Leu Tyr
 35 40 45
 Arg Phe Met Leu Met Cys Lys Asn Glu Leu Gly Leu Thr Asp Ala Ala
 50 55 60
 Leu Phe Ser Ile Ser Glu Ile Tyr Lys Pro Ser Thr Ala Pro Leu Val
 65 70 75 80
 Arg Ala Leu Gln Thr Ile Glu Leu Leu Leu Lys Lys Tyr Glu Val Ser
 85 90 95
 Asn Thr Thr Lys Ser Ser Ser Thr Pro Ser Pro Ser Thr Asp Asp Asn
 100 105 110
 Val Pro Thr Gly Thr Leu Asn Ser Leu Ile Ala Ser Gly Arg Arg Val
 115 120 125
 Thr Ala Glu Leu Tyr Glu Thr Glu Leu Lys Tyr Ile Gln Asp Leu Glu
 130 135 140
 Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln Lys Gln Ile Leu Ser
 145 150 155 160
 Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu Ile Leu Asp
 165 170 175
 Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu Ser Leu Pro
 180 185 190
 Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ile Ala Leu Glu Glu Gly
 195 200 205
 Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn Ala Gln Gln
 210 215 220
 Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala Asn Leu Leu
 225 230 235 240
 Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro Ile Gln Arg
 245 250 255
 Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys Gly Thr Pro
 260 265 270
 Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met Ala Cys Val
 275 280 285
 Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg Ile His Glu Asn
 290 295 300
 Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile Asp Trp Lys Gly
 305 310 315 320
 Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp Val Val Asn
 325 330 335
 Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val Tyr Leu Phe Glu
 340 345 350

Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu Lys Arg Gln Ala
 355 360 365
 Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu Asp Ser Leu Gln
 370 375 380
 Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr Val Val Pro Asn
 385 390 395 400
 His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg Gly Asp Pro
 405 410 415
 Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu Glu Ser His Lys
 420 425 430
 Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys Asn Glu His Gly
 435 440 445
 Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro Ala Asn Pro Val
 450 455 460
 Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly Tyr Asn Ser Ser Asp
 465 470 475 480
 Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn Val Asn Ser Pro
 485 490 495
 Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro Phe Thr Lys Thr
 500 505 510
 Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Thr Asp Glu Arg Pro Ser
 515 520 525
 Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val Gly Thr Ser Ser Leu
 530 535 540
 Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn Asp Ser Ser Ser
 545 550 555 560
 Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser Gln Val Asn Ser
 565 570 575
 Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val
 580 585 590
 Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr
 595 600 605
 Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp
 610 615 620
 Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys
 625 630 635 640
 Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser
 645 650 655
 Ser Ser Thr Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys
 660 665 670
 Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His

675 680 685
 Asp Ile Thr Phe Asp Glu Leu Leu Ala Lys Val Glu His Lys Ile Lys
 690 695 700
 Leu Cys Gly Ile Leu Lys Gln Ala Val Pro Phe Arg Val Arg Leu Lys
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 Tyr Val Asp Glu Asp Gly Asp Phe Ile Thr Ile Thr Ser Asp Glu Asp
 725 730 735
 Val Leu Met Ala Phe Glu
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18

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 <211> 76
 <212> PRT
 <213> Candida albicans

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Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
 20 25 30

Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

35 40 45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60
Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr
65 70 75
<210> 35 <211> 19 <212> PRT <213> Candida albicans <400> 35
Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
1 5 10 15
Lys Ser Val
<210> 36
<211> 73
<212> PRT
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Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15
Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30
Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
35 40 45
Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
50 55 60
Ile Ile Asp Val Ile Asn Lys Leu Leu
65 70
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<211> 73
<212> PRT
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Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met
65 70